

SEQUENCE LISTING

<110> Beerli, Roger R.  
Bachmann, Martin F.

<120> Modified Polypeptides For Targeting Cell-Entry of the Adenoviruses of Subtype B

<130> 1700.0640000/BJD/WBC

<150> EP03011184.3  
<151> 2003-05-27

<150> PCT/EP2004/005762  
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<170> PatentIn version 3.1

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gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca	300
tatatacggg atccttttaa tggccaagca gtccctgcaa atgggactta cgagtttggt	360
tatcagatgc actttatttg taatgagggt tattacttaa ttggtgaaga aattctatat	420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt	480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca cctttagtga agtagaagta	540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt	600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct	660

ccagagtgtgta aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca 720  
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt 780  
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt 840  
ccaaagtgtc ttaaaggtcc taggcctact tacaagcctc cagtctcaaa ttatccagga 900  
tatacctaaac ctgaggaagg aatacttgac agtttggatg tt 942

<210> 13  
<211> 314  
<212> PRT  
<213> homo sapiens

<400> 13

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe  
1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser  
20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly  
35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys  
50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys  
65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg  
85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro  
100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn  
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys  
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val  
145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser  
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp

180	185	190
Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile		
195	200	205
Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys		
210	215	220
Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser		
225	230	235
Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys		
	245	250
Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser		
	260	265
Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Gly Pro Arg		
	275	280
Pro Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro		
	290	295
Glu Glu Gly Ile Leu Asp Ser Leu Asp Val		
305	310	

<210> 14  
 <211> 945  
 <212> DNA  
 <213> homo sapiens

<400> 14	
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tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta	180
gattataagt gtaaaaaagg atacttctat atacctcttc ttgccacca tactatttgt	240
gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca	300
tatatacggg atccttttaa tggccaagca gtccctgcaa atgggactta cgagtttggt	360
tatcagatgc actttatttg taatgagggt tattacttaa ttgggtgaaga aattctatat	420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc ccccaatatg tgaaaagggt	480
ttgtgtacac cacctccaaa aataaaaaat ggagaacaca cctttagtga agtagaagta	540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt	600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct	660

ccagagtgtgta aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca 720  
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt 780  
tacctcgatg gcagcgacac aattgtctgt .gacagtaaca gtacttggga tccccagtt 840  
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca 900  
ggatataccta aacctgagga aggaatactt gacagtttgg atgtt 945

<210> 15  
<211> 315  
<212> PRT  
<213> homo sapiens

<400>. 15

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe  
1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser  
20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly  
35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys  
50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys  
65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg  
85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro  
100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn  
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys  
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val  
145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Glu His Thr Phe Ser  
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp

180	185	190
Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile		
195	200	205
Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys		
210	215	220
Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser		
225	230	235
Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys		
	245	250
Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser		
	260	265
Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr		
	275	280
Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Tyr Pro Lys		
	290	295
Pro Glu Glu Gly Ile Leu Asp Ser Leu Asp Val		
305	310	315

<210> 16  
 <211> 987  
 <212> DNA  
 <213> homo sapiens

<400> 16	
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ctggcggcca tgggtgttgc gctgtactcc ttctccgatg cctgtgagga gccaccaaca	120
tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta	180
gattataagt gtaaaaaagg atacttctat atacctctc ttgccacca tactatttgt	240
gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca	300
tatatacggg atccttttaa tggccaagca gtccttgcaa atgggactta cgagtttggt	360
tatcagatgc actttatttg taatgagggt tattacttaa ttgggtgaaga aattctatat	420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt	480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca cctttagtga agtagaagta	540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt	600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct	660

ccagagtgtgta aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca 720  
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt 780  
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt 840  
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca 900  
ggtcctaggc ctacttataa gcctccagtc tcaaattatc caggatatcc taaacctgag 960  
gaaggaatac ttgacagttt ggatggt 987

<210> 17  
<211> 329  
<212> PRT  
<213> homo sapiens

<400> 17

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe  
1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser  
20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly  
35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys  
50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys  
65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg  
85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro  
100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn  
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys  
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val  
145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser  
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp  
180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile  
195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys  
210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser  
225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys  
245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser  
260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr  
275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro  
290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu  
305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val  
325

<210> 18  
<211> 1671  
<212> DNA  
<213> artificial sequence

<220>  
<223> Construct encoding a fusion polypeptide between the extracellular domain of CD46 at the N-terminus and a human Fc-gamma3 domain at the C-terminus

<400> 18  
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tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta 180  
gattataagt gtaaaaaagg atacttctat atacctcctc ttgccacca tactatttgt 240  
gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca 300



tatatacggg atcctttaa tggccaagca gtccctgcaa atgggactta cgagtttgg	360
tatcagatgc actttatttg taatgagggg tattacttaa ttggtgaaga aattctatat	420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt	480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca ctttagtga agtagaagta	540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt	600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct	660
ccagagtgtg aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca	720
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt	780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt	840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca	900
ggctcctaggc ctacttacia gcctccagtc tcaaattatc caggatatcc taaacctgag	960
gaaggaatac ttgacagttt ggatgttaag cttactcaca catgcccacc gtgcccagca	1020
cctgaagccg agggggcacc gtcagtcctc ctcttcccc caaaacccaa ggacaccctc	1080
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct	1140
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcca gacaaagccg	1200
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag	1260
gactggctga atggcaagga gtacaagtgc aagggtctcca acaaagccct cccagcctcc	1320
atcgagaaaa ccatctcaa agccaaaggg cagccccgag aaccacaggt gtacaccctg	1380
ccccatccc gggatgagct gaccaagaac cagggtcagcc tgacctgcct ggtcaaaggc	1440
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac	1500
aagaccacgc ctcccgtgtt ggactccgac ggctccttct tcctctacag caagctcacc	1560
gtggacaaga gcagggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct	1620
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<210> 19  
 <211> 556  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> fusion polypeptide between the extracellular domain of CD46 at the N-terminus and a human Fc-gamma3 domain at the C-terminus  
 <400> 19

Met	Glu	Pro	Pro	Gly	Arg	Arg	Glu	Cys	Pro	Phe	Pro	Ser	Trp	Arg	Phe
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Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser  
 20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly  
 35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys  
 50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys  
 65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg  
 85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro  
 100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn  
 115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys  
 130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val  
 145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser  
 165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp  
 180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile  
 195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys  
 210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser  
 225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys  
 245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser  
 260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr  
 275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro  
 290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu  
 305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val Lys Leu Thr His Thr Cys Pro  
 325 330 335

Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe  
 340 345 350

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 355 360 365

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 370 375 380

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 385 390 395 400

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 405 410 415

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 420 425 430

Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala  
 435 440 445

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 450 455 460

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 465 470 475 480

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 485 490 495

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 500 505 510

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

515

520

525

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 530 535 540

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 545 550 555

<210> 20  
 <211> 1746  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> Construct encoding a fusion polypeptide between the extracellular domain of CD46 at the N-terminus and the scFv FRP5 against ErbB-2 at the C-terminus

<400> 20  
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 tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta 180  
 gattataagt gtaaaaaagg atacttctat atacctcttc ttgccacca tactatttgt 240  
 gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca 300  
 tatatacggg atcctttaa tggccaagca gtccctgcaa atgggactta cgagtttggt 360  
 tatcagatgc actttatttg taatgagggt tattacttaa ttggtgaaga aattctatat 420  
 tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt 480  
 ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca cctttagtga agtagaagta 540  
 tttagagtac ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt 600  
 tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct 660  
 ccagagtgta aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca 720  
 ggatttgga aaaaatttta ctacaaagca acagttatgt ttgaatgcca taagggtttt 780  
 tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt 840  
 ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca 900  
 ggtcctaggc ctacttacaa gcctccagtc tcaaattatc caggatatcc taaacctgag 960  
 gaaggaatac ttgacagttt ggatgttggc ggccgctctc aggtacaact gcagcagtct 1020  
 ggacctgaac tgaagaagcc tggagagaca gtcaagatct cctgcaaggc ctctgggtat 1080  
 cctttcacia actatggaat gaactgggtg aagcaggctc caggacaggg tttaaagtgg 1140  
 atgggctgga ttaacacttc cactggagag tcaacatttg ctgatgactt caagggacgg 1200

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tactgggggcc aaggggaccac ggtcaccggt tcctctggcg gtggcggttc tgggtggcggt 1380
ggctccggcg gtggcggttc tgacatccag ctgacccagt ctcacaaatt cctgtccact 1440
tcagtaggag acaggggtcag catcacctgc aaggccagtc aggatgtgta taatgctggt 1500
gcctgggtatc aacagaaacc aggacaatct cctaaacttc tgatttactc ggcatectcc 1560
cggtacactg gagtcccttc tcgcttcact ggcagtggct ctggggccgga tttcactttc 1620
accatcagca gtgtgcaggc tgaagacctg gcagtttatt tctgtcagca acattttcgt 1680
actccattca cgttcggctc ggggacaaaa ttggagatcg actacaagga tgacgacgac 1740
aagtag 1746

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<210> 21
<211> 581
<212> PRT
<213> artificial sequence

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<220>
<223> fusion polypeptide between the extracellular domain of CD46 at th
      e N-terminus and the scFv FRP5 against ErbB-2 at the C-terminus

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```

<400> 21

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Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1          5          10          15

```

```

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
          20          25          30

```

```

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
          35          40          45

```

```

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
          50          55          60

```

```

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
65          70          75          80

```

```

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
          85          90          95

```

```

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
          100          105          110

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```

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
          115          120          125

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Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys  
 130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val  
 145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser  
 165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp  
 180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile  
 195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys  
 210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser  
 225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys  
 245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser  
 260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr  
 275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro  
 290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu  
 305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val Gly Gly Arg Ser Gln Val Gln  
 325 330 335

Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Lys  
 340 345 350

Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn  
 355 360 365

Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile

370

375

380

Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp Asp Phe Lys Gly Arg  
 385 390 395 400

Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile  
 405 410 415

Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr Phe Cys Ala Arg Trp  
 420 425 430

Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly Gln Gly Thr Thr Val  
 435 440 445

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
 450 455 460

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His Lys Phe Leu Ser Thr  
 465 470 475 480

Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val  
 485 490 495

Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
 500 505 510

Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr Gly Val Pro Ser Arg  
 515 520 525

Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr Phe Thr Ile Ser Ser  
 530 535 540

Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Phe Arg  
 545 550 555 560

Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asp Tyr Lys  
 565 570 575

Asp Asp Asp Asp Lys  
 580